

<!--StartFragment-->RESULT 1

Q9ZRC7_ALNGL

ID Q9ZRC7_ALNGL Unreviewed; 99 AA.
 AC Q9ZRC7;
 DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1999, sequence version 1.
 DT 24-JUL-2007, entry version 22.
 DE Actinorizal nodulin AgNOD-GHRP.
 GN Name=agNt84;
 OS *Alnus glutinosa* (Alder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Fagales; Betulaceae; *Alnus*.
 OX NCBI_TaxID=3517;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Root nodules;
 RA Dobritsa S.V., Mullin B.C.;
 RT "In vitro expression of actinorhizal nodulin AgNOD-GHRP and
 RT demonstration of its toxicity ot *Escherichia coli*.";
 RL (In) Stacey G., Mullin B.C., Gresshoff P.M. (eds.);
 RL THE BIOLOGY OF PLANT-MICROBE INTERACTIONS: PROCEEDINGS OF THE 8TH
 RL INTERNATIONAL SYMPOSIUM ON MOLECULAR PLANT-MICROBE INTERACTIONS,
 RL pp.1-1, Unknown Publisher (1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Root nodules;
 RA Twigg P.G.;
 RT "Isolation of a nodule-specific cDNA encoding a putative glycine-rich
 RT protein from *Alnus glutinosa*.";
 RL Thesis (1993), The University of Tennessee, Knoxville, TN, USA.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Root nodules;
 RA Pawlowski K., Twigg P.G., Dobritsa S.V., Guan C., Mullin B.C.;
 RT "A nodule-specific gene family from *Alnus glutinosa* encodes glycine
 RT and histidine-rich proteins expressed in the early stages of
 RT actinorhizal nodule development.";
 RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL; U69156; AAD00171.1; -; mRNA.
 DR InterPro; IPR010800; GRP.
 DR Pfam; PF07172; GRP; 1.
 PE 4: Predicted;
 SQ SEQUENCE 99 AA; 10567 MW; 2ACBE4D57C070E83 CRC64;

Query Match 100.0%; Score 99; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.4e-89;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGYSKTFLLLGLAFVLLISSDVSASELAVAAQTKENMQTDGVEEDKYHGHRHVHGHGH 60
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 Db 1 MGYSKTFLLLGLAFVLLISSDVSASELAVAAQTKENMQTDGVEEDKYHGHRHVHGHGH 60
 Qy 61 GHVHGNGNEHGHGHHHGRGHPGHGAAADETETETETNQ 99
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 Db 61 GHVHGNGNEHGHGHHHGRGHPGHGAAADETETETETNQ 99

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